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[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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General information about the entry

Entry name	**NEUL_HUMAN**
Primary accession number	**Q9BYT8**
Secondary accession number	Q9ULJ4
Entered in Swiss-Prot in	Release 41, February 2003
Sequence was last modified in	Release 41, February 2003
Annotations were last modified in	Release 42, September 2003

Name and origin of the protein

Protein name	**Neurolysin, mitochondrial [Precursor]**
Synonyms	**EC 3.4.24.16** **Neurotensin endopeptidase** **Mitochondrial oligopeptidase M** **Microsomal endopeptidase** **MEP**
Gene name	**NLN** or **KIAA1226**
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

[1] SEQUENCE FROM NUCLEIC ACID.
Chen J.M., Rawlings N.D., Barrett A.J.;
"Cloning and sequencing of human neurolysin, an oligopeptidase of family M3.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

[2] SEQUENCE FROM NUCLEIC ACID.
TISSUE=Brain;
MEDLINE=20039619; PubMed=10574462; [NCBI, ExPASy, EBI, Israel, Japan]
Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999).

Comments

- ***FUNCTION***: Hydrolyzes oligopeptides such as neurotensin, bradykinin, dynorphin A, etc. *(By similarity)*.
- ***CATALYTIC ACTIVITY***: Preferential cleavage in neurotensin: 10-Pro-|-Tyr-11.
- ***COFACTOR***: BINDS 1 ZINC ION *(By similarity)*.
- ***SUBCELLULAR LOCATION***: MITOCHONDRIAL INTERMEMBRANE SPACE AND ALSO CYTOPLASMIC *(By similarity)*.
- ***SIMILARITY***: BELONGS TO PEPTIDASE FAMILY M3.

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Cross-references

EMBL	AJ300837; CAC27329.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AB033052; BAA86540.2; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
Genew	HGNC:16058; NLN.
CleanEx	HGNC:16058; NLN.
Ensembl	Q9BYT8; Homo sapiens. [Entry / Contig view]
HUGE	KIAA1226.
InterPro	IPR001567; Peptidase_M3. IPR006025; Zn_MTpeptdse. Graphical view of domain structure.
Pfam	PF01432; Peptidase_M3; 1.
PROSITE	PS00142; ZINC_PROTEASE; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q9BYT8.
ProtoNet	Q9BYT8.
ProtoMap	Q9BYT8.
PRESAGE	Q9BYT8.
DIP	Q9BYT8.
ModBase	Q9BYT8.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Metalloprotease; **Hydrolase**; **Zinc**; **Mitochondrion**; **Transit peptide**.

Features

Feature table viewer

Key	From	To	Length	Description
TRANSIT	1	37	37	MITOCHONDRION (*BY SIMILARITY*).
CHAIN	38	704	667	NEUROLYSIN.
METAL	497	497		ZINC (CATALYTIC) (*BY SIMILARITY*).
ACT_SITE	498	498		*BY SIMILARITY*.
METAL	501	501		ZINC (CATALYTIC) (*BY SIMILARITY*).
METAL	504	504		ZINC (CATALYTIC) (*BY SIMILARITY*).

Sequence information

Length: **704 AA** [This is the length of the unprocessed precursor]	Molecular weight: **80651 Da** [This is the MW of the unprocessed precursor]	CRC64: **80136688D79BBEDF** [This is a checksum on the sequence]

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        10         20         30         40         50         60
         |          |          |          |          |          |
MIARCLLAVR SLRRVGGSRI LLRMTLGREV MSPLQAMSSY TVAGRNVLRW DLSPEQIKTR

        70         80         90        100        110        120
         |          |          |          |          |          |
TEELIVQTKQ VYDAVGMLGI EEVTYENCLQ ALADVEVKYI VERTMLDFPQ HVSSDKEVRA

       130        140        150        160        170        180
         |          |          |          |          |          |
ASTEADKRLS RFDIEMSMRG DIFERIVHLQ ETCDLGKIKP EARRYLEKSI KMGKRNGLHL

       190        200        210        220        230        240
         |          |          |          |          |          |
PEQVQNEIKS MKKRMSELCI DFNKNLNEDD TFLVFSKAEL GALPDDFIDS LEKTDDDKYK

       250        260        270        280        290        300
         |          |          |          |          |          |
ITLKYPHYFP VMKKCCIPET RRRMEMAFNT RCKEENTIIL QQLLPLRTKV AKLLGYSTHA

       310        320        330        340        350        360
         |          |          |          |          |          |
DFVLEMNTAK STSRVTAFLD DLSQKLKPLG EAEREFILNL KKKECKDRGF EYDGKINAWD

       370        380        390        400        410        420
         |          |          |          |          |          |
LYYYMTQTEE LKYSIDQEFL KEYFPIEVVT EGLLNTYQEL LGLSFEQMTD AHVWNKSVTL

       430        440        450        460        470        480
         |          |          |          |          |          |
YTVKDKATGE VLGQFYLDLY PREGKYNHAA CFGLQPGCLL PDGSRMMAVA ALVVNFSQPV

       490        500        510        520        530        540
         |          |          |          |          |          |
AGRPSLLRHD EVRTYFHEFG HVMHQICAQT DFARFSGTNV ETDFVEVPSQ MLENWVWDVD

       550        560        570        580        590        600
         |          |          |          |          |          |
SLRRLSKHYK DGSPIADDLL EKLVASRLVN TGLLTLRQIV LSKVDQSLHT NTSLDAASEY

       610        620        630        640        650        660
         |          |          |          |          |          |
AKYCSEILGV AATPGTNMPA TFGHLAGGYD GQYYGYLWSE VFSMDMFYSC FKKEGIMNPE

       670        680        690        700
         |          |          |          |
VGMKYRNLIL KPGGSLDGMD MLHNFLKREP NQKAFLMSRG LHAP
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Q9BYT8 in FASTA format

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1: Br J Pharmacol 1997 Jun;121(4):705-10 Related Articles, Links

Effect of a novel selective and potent phosphinic peptide inhibitor of endopeptidase 3.4.24.16 on neurotensin-induced analgesia and neuronal inactivation.

Vincent B, Jiracek J, Noble F, Loog M, Roques B, Dive V, Vincent JP, Checler F.

IPMC du CNRS, UPR411, Valbonne, France.

1. We have examined a series of novel phosphinic peptides as putative potent and selective inhibitors of endopeptidase 3.4.24.16. 2. The most selective inhibitor, Pro-Phe-psi(PO2CH2)-Leu-Pro-NH2 displayed a Ki value of 12 nM towards endopeptidase 3.4.24.16 and was 5540 fold less potent on its related peptidase endopeptidase 3.4.24.15. Furthermore, this inhibitor was 12.5 less potent on angiotensin-converting enzyme and was unable to block endopeptidase 3.4.24.11, aminopeptidases B and M, dipeptidylaminopeptidase IV and proline endopeptidase. 3. The effect of Pro-Phe-psi(PO2CH2)-Leu-Pro-NH2, in vitro and in vivo, on neurotensin metabolism in the central nervous system was examined. 4. Pro-Phe-psi(PO2CHH2)-Leu-Pro-NH2 dose-dependently inhibited the formation of neurotensin 1-10 and concomittantly protected neurotensin from degradation by primary cultured neurones from mouse embryos. 5. Intracerebroventricular administration of Pro-Phe-psi(PO2CH2)-Leu-Pro-NH2 significantly potentiated the neurotensin-induced antinociception of mice in the hot plate test. 6. Altogether, our study has established Pro-Phe-psi(PO2CH2)-Leu-Pro-NH2 as a fully selective and highly potent inhibitor of endopeptidase 3.4.24.16 and demonstrates, for the first time, the contribution of this enzyme in the central metabolism of neurotensin.

PMID: 9208137 [PubMed - indexed for MEDLINE]